

SEQUENCE PROTOCOL

<110> Degussa AG

5 <120> New nucleotide sequences which code for the lysR2 gene

<130> 000181 BT

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<170> PatentIn Ver. 2.1

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<212> DNA

<213> Corynebacterium glutamicum

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<222> (232)..(1161)

<223> lysR2 gene

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cctcgacattt gctatctatt gcttggctca tggagttcat catgcgccaa cagcaaataat 180

tagtaaaatg ttagaaatag ctgttttga ttcactttgt gcatgttaggc t gtg acc 237
Met Thr
1

35

atg ggc aac gac ggc gga gac ctg cga atc gac gac cta cgc agc ttc 285
Met Gly Asn Asp Gly Gly Asp Leu Arg Ile Asp Asp Leu Arg Ser Phe
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40

att tca gtc gct caa tca ggc cac ctc acc gaa act gcc gaa aga tta 333
Ile Ser Val Ala Gln Ser Gly His Leu Thr Glu Thr Ala Glu Arg Leu
20 25 30

45

ggc atc ccg cag ccc aca ctt tcc aga cga atc agc cga gtg gaa aaa 381
Gly Ile Pro Gln Pro Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys
35 40 45 50

50

cac gca ggc acc cca ctt ttc gac cgc gcc ggc cgc aaa ctc gtc ctc 429
His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu
55 60 65

55

aac caa cga ggc cac gcc ttc ctc aac cac gcc agc gcc atc gtc gca 477
Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala
70 75 80gaa ttc aac tcc gcc gca act gaa atc aaa cgc ctc atg gac cca gaa 525
Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu
85 90 95

| | |
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| aaa ggc aca atc cga ctg gac ttc atg cat tcc ttg ggc act tgg atg | 573 |
| Lys Gly Thr Ile Arg Leu Asp Phe Met His Ser Leu Gly Thr Trp Met | |
| 100 105 110 | |
| 5 | |
| gtc ccc gaa ctt atc cga aca ttc cgc gcc gaa cac ccc aac gta gaa | 621 |
| Val Pro Glu Leu Ile Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu | |
| 115 120 125 130 | |
| 10 ttc caa ctc cac caa gcg gca gca atg ctc ctg gta gat cgt gtt ttg | 669 |
| Phe Gln Leu His Gln Ala Ala Met Leu Leu Val Asp Arg Val Leu | |
| 135 140 145 | |
| 15 gct gat gaa act gac ctc gca tta gtt ggc ccc aaa cct gcc gag gtt | 717 |
| Ala Asp Glu Thr Asp Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val | |
| 150 155 160 | |
| 20 ggt acc tct tta ggg tgg gcg cca ctg ctt cgt caa cga ctt gcc cta | 765 |
| Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu | |
| 165 170 175 | |
| 25 gct gtt ccc gca gat cac cgg ctt gcc tcc ttt tct ggc caa gga gaa | 813 |
| Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu | |
| 180 185 190 | |
| 30 ttg ccg ttg att act gcg gcg gaa gaa cct ttc gtg gcg atg cga gca | 861 |
| Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala | |
| 195 200 205 210 | |
| 35 ggt ttc ggc acc cga ctc ctc atg gat gca tta gcc gaa gaa gcc ggt | 909 |
| Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly | |
| 215 220 225 | |
| 40 ttt gtt ccc aat gtg gtt ttc gaa tcc atg gaa ctc acc acc gtc gca | 957 |
| Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr Val Ala | |
| 230 235 240 | |
| 45 ggg ctt gtc agc gca ggt ctc ggc gtt ggt gtg gtt ccg atg gat gat | 1005 |
| Gly Leu Val Ser Ala Gly Leu Gly Val Gly Val Val Pro Met Asp Asp | |
| 245 250 255 | |
| 50 ccg tac ctt ccc aca gtg gga atc gtg caa cgc cca ctt agt cca ccc | 1053 |
| Pro Tyr Leu Pro Thr Val Gly Ile Val Gln Arg Pro Leu Ser Pro Pro | |
| 260 265 270 | |
| 55 gct tat agg gaa cta ggt ttg gtg tgg cga ctc aac gcg ggg ccg gca | 1101 |
| Ala Tyr Arg Glu Leu Gly Leu Val Trp Arg Leu Asn Ala Gly Pro Ala | |
| 275 280 285 290 | |
| 50 cct gcg gtg gat aac ttc cgg aag ttc gtg gcg gga tcg agg tat gca | 1149 |
| Pro Ala Val Asp Asn Phe Arg Lys Phe Val Ala Gly Ser Arg Tyr Ala | |
| 295 300 305 | |
| 55 tta gaa gag ggc tgagctgtaa gtgtcgtggg tgccgttta aggggttgag | 1201 |
| Leu Glu Glu Gly | |
| 310 | |
| ttttcccgat gactaggagt tggccagat tgtgcgttag gggccctag gggcgattct | 1261 |

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 35 40 45

20 20 Glu Lys His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu
 50 55 60

25 25 Val Leu Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile
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 85 90 95

30 30 Pro Glu Lys Gly Thr Ile Arg Leu Asp Phe Met His Ser Leu Gly Thr
 100 105 110

Trp Met Val Pro Glu Leu Ile Arg Thr Phe Arg Ala Glu His Pro Asn
 115 120 125

35 35 Val Glu Phe Gln Leu His Gln Ala Ala Ala Met Leu Leu Val Asp Arg
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Val Leu Ala Asp Glu Thr Asp Leu Ala Leu Val Gly Pro Lys Pro Ala
 40 145 150 155 160

Glu Val Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu
 165 170 175

45 45 Ala Leu Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln
 180 185 190

Gly Glu Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met
 195 200 205

50 50 Arg Ala Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu
 210 215 220

Ala Gly Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr
 55 225 230 235 240

Val Ala Gly Leu Val Ser Ala Gly Leu Gly Val Gly Val Val Pro Met
 245 250 255

Asp Asp Pro Tyr Leu Pro Thr Val Gly Ile Val Gln Arg Pro Leu Ser
260 265 270

5 Pro Pro Ala Tyr Arg Glu Leu Gly Leu Val Trp Arg Leu Asn Ala Gly
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tccgaacatt ccgcgcccga caccggaaac tagaattcca actccaccaa gcggcagcaa 180
tgctccttgtt agatcggtt ttggctgatg aaactgaccc cgcatttagtt ggccccaaac 240
ctgcccgggt tggtacctct ttagggtggg cgccactgct tcgtcaacga cttggccctag 300
30 ctgtccccgc agatcaccgg ctgcctcct tttctggcca aggagaattt ccgttgattt 360
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The following figures are attached:

Figure 1: Map of the plasmid pCR2.1lysR2int.

The abbreviations and designations used have the following meaning.

KmR: Kanamycin resistance gene

EcoRI: Cleavage site of the restriction enzyme EcoRI

lysR2int: Internal fragment of the lysR2 gene

ColE1 ori: Replication origin of the plasmid ColE1

SEQUENZPROTOKOLL

<110> Degussa AG

5 <120> Neue für das lysR2-Gen kodierende Nukleotidsequenzen

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15 <170> PatentIn Ver. 2.1

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cctcgacctt gctatctatt gcttggctca tggagttcat catgcgccaa cagcaaataat 180

tagtaaaatg ttagaaatag ctgttttga ttcactttgt gcatgttaggc t gtg acc 237
Met Thr
135 atg ggc aac gac ggc gga gac ctg cga atc gac gac cta cgc agc ttc 285
Met Gly Asn Asp Gly Gly Asp Leu Arg Ile Asp Asp Leu Arg Ser Phe

5

10

15

40 att tca gtc gct caa tca ggc cac ctc acc gaa act gcc gaa aga tta 333
Ile Ser Val Ala Gln Ser Gly His Leu Thr Glu Thr Ala Glu Arg Leu
20 25 3045 ggc atc ccg cag ccc aca ctt tcc aga cga atc agc cga gtg gaa aaa 381
Gly Ile Pro Gln Pro Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys
35 40 45 5050 cac gca ggc acc cca ctt ttc gac cgc gcc ggc cgc aaa ctc gtc ctc 429
His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu
55 60 6555 aac caa cga ggc cac gcc ttc ctc aac cac gcc agc gcc atc gtc gca 477
Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala
70 75 80gaa ttc aac tcc gcc gca act gaa atc aaa cgc ctc atg gac cca gaa 525
Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu
85 90 95

| | | |
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| | aaa ggc aca atc cga ctg gac ttc atg cat tcc ttg ggc act tgg atg | 573 |
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| | gtc ccc gaa ctt atc cga aca ttc cgc gcc gaa cac ccc aac gta gaa | 621 |
| | Val Pro Glu Leu Ile Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu | |
| | 115 120 125 130 | |
| 10 | ttc caa ctc cac caa gcg gca gca atg ctc ctg gta gat cgt gtt ttg | 669 |
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| | Ala Asp Glu Thr Asp Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val | |
| | 150 155 160 | |
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| | Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu | |
| | 165 170 175 | |
| | gct gtt ccc gca gat cac cgg ctt gcc tcc ttt tct ggc caa gga gaa | 813 |
| | Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu | |
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| 30 | ggt ttc ggc acc cga ctc ctc atg gat gca tta gcc gaa gaa gcc ggt | 909 |
| | Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly | |
| | 215 220 225 | |
| 35 | ttt gtt ccc aat gtg gtt ttc gaa tcc atg gaa ctc acc acc gtc gca | 957 |
| | Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr Val Ala | |
| | 230 235 240 | |
| 40 | ggg ctt gtc agc gca ggt ctc ggc gtt ggt gtg gtt ccg atg gat gat | 1005 |
| | Gly Leu Val Ser Ala Gly Leu Gly Val Gly Val Val Pro Met Asp Asp | |
| | 245 250 255 | |
| 45 | ccg tac ctt ccc aca gtg gga atc gtg caa cgc cca ctt agt cca ccc | 1053 |
| | Pro Tyr Leu Pro Thr Val Gly Ile Val Gln Arg Pro Leu Ser Pro Pro | |
| | 260 265 270 | |
| | gct tat agg gaa cta ggt ttg gtg tgg cga ctc aac gcg ggg ccg gca | 1101 |
| | Ala Tyr Arg Glu Leu Gly Leu Val Trp Arg Leu Asn Ala Gly Pro Ala | |
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| 50 | cct gcg gtg gat aac ttc cgg aag ttc gtg gcg gga tcg agg tat gca | 1149 |
| | Pro Ala Val Asp Asn Phe Arg Lys Phe Val Ala Gly Ser Arg Tyr Ala | |
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| | Leu Glu Glu Gly | |
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20 Glu Lys His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu
 50 55 60

25 Val Leu Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile
 65 70 75 80

Val Ala Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp
 85 90 95

30 Pro Glu Lys Gly Thr Ile Arg Leu Asp Phe Met His Ser Leu Gly Thr
 100 105 110

Trp Met Val Pro Glu Leu Ile Arg Thr Phe Arg Ala Glu His Pro Asn
 35 115 120 125

Val Glu Phe Gln Leu His Gln Ala Ala Met Leu Leu Val Asp Arg
 130 135 140

40 Val Leu Ala Asp Glu Thr Asp Leu Ala Leu Val Gly Pro Lys Pro Ala
 145 150 155 160

Glu Val Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu
 165 170 175

45 Ala Leu Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln
 180 185 190

Gly Glu Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met
 50 195 200 205

Arg Ala Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu
 210 215 220

Ala Gly Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr
 55 225 230 235 240

Val Ala Gly Leu Val Ser Ala Gly Leu Gly Val Gly Val Val Pro Met
 245 250 255

Asp Asp Pro Tyr Leu Pro Thr Val Gly Ile Val Gln Arg Pro Leu Ser
 260 265 270

5 Pro Pro Ala Tyr Arg Glu Leu Gly Leu Val Trp Arg Leu Asn Ala Gly
 275 280 285

Pro Ala Pro Ala Val Asp Asn Phe Arg Lys Phe Val Ala Gly Ser Arg
 290 295 300

10 Tyr Ala Leu Glu Glu Gly
 305 310

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20 <220>
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 tccgaacatt ccgcgcggaa cacccaaacg tagaattcca actccaccaa gcggcagcaa 180
 tgctccttgtt agatcgtgtt ttggctgatg aaactgaccc cgcattagtt ggccccaaac 240
 ctgcccgggt tggtacctt ttagggtggg cggcactgct tcgtcaacga cttgccctag 300
 30 ctgttcccgc agatcacccg cttgcctctt tttctggcca aggagaattt ccgttgatta 360
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<400> 5
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